HDM2-INHIBITOR COMPLEXES AND USES THEREOF

ABSTRACT OF THE DISCLOSURE

The present invention includes crystallized HDM2 peptides as well as descriptions of the X-ray diffraction patterns of the crystals. The diffraction patterns allow the three dimensional structure of HDM2 to be determined at atomic resolution so that ligand binding sites on HDM2 can be identified and the interactions of ligands with HDM2 amino acid residues can be modeled. Models prepared using such maps permit the design of ligands which can function as active agents which include, but are not limited to, those that function as inhibitors of MDM2 and HDM2 oncoproteins.